conjoining at least one homologous recombination site to a plurality of the functionally similar subsequences, thereby producing a plurality of recombination cassettes; and,

recombining the recombination cassettes, or fragments thereof, at the recombination sites, thereby producing a plurality of permutations of the recombination cassettes within a plurality of resulting recombinant nucleic acids.

Please **add** the following claims:

153. (New) The method of claim 51, further comprising recombining one or more of the plurality of recombinant nucleic acids with one or more additional nucleic acid.

154. (New) The method of claim 51, further comprising fragmenting the recombination cassettes with a nuclease prior to said recombining step, wherein said recombining step is performed by primerless PCR.

155. (New) The method of claim 51, wherein the at least one nucleic acid comprises one or more sequence produced by in vitro sequence recombination.

156. (New) The method of claim 51, wherein the at least one nucleic acid comprises one or more sequences produced by recursive in vitro recombination.

157. (New) The method of claim 51, wherein the at least one nucleic acid is produced by in vivo recombination.

158. (New) The method of claim 51, wherein the at least one nucleic acid is produced by recursive in vivo sequence recombination.

159. (New) The method of claim 51, wherein the plurality of recombination cassettes comprise subsequences which are allelic or species variants.

160. (New) The method of claim 51, wherein the at least one nucleic acid is selected from one or more libraries of nucleic acids derived from one or more of: a bacteria, an Alcaligenes, a Zoogloea, a Rhizobium, a Bacillus, an Azobacter, or a eukaryote.

161. (New) The method of claim 51 wherein, the gene cluster encodes a multi-enzyme pathway.

162. (New) The method of claim 161, further comprising recombining one or more of the plurality of recombinant nucleic acids with one or more additional nucleic acid.

163. (New) The method of claim 161, further comprising fragmenting the recombination cassettes with a nuclease prior to said recombining step, wherein said recombining step is performed by primerless PCR.

164. (New) The method of claim 161, wherein the at least one nucleic acid comprises one or more sequence produced by in vitro sequence recombination.

165. (New) The method of claim 161, wherein the at least one nucleic acid comprises one or more sequences produced by recursive in vitro recombination.

166. (New) The method of claim 161, wherein the at least one nucleic acid is produced by in vivo recombination.

167. (New) The method of claim 161, wherein the at least one nucleic acid is produced by recursive in vivo sequence recombination.

168. (New) The method of claim 161, wherein the plurality of recombination cassettes comprise subsequences which are allelic or species variants.

169. (New) The method of claim 161, wherein the at least one nucleic acid is selected from one or more libraries of nucleic acids derived from one or more of: a bacteria, an Alcaligenes, a Zoogloea, a Rhizobium, a Bacillus, an Azobacter, or a eukaryote.

In accordance with the requirements of 37 C.F.R. § 1.121, a marked up version showing the changes to the claims, is attached herewith as Appendix A. For the Examiner's convenience, a complete claim set of the currently pending claims is also submitted herewith as Appendix B.

These amendments are made without prejudice and are not to be construed as abandonment of the previously claimed subject matter or agreement with any objection or rejection of record.

**REMARKS**

CONCERNING THE CHANGE TO THE PRIORITY CLAIM

The present application claims priority to U.S. patent application Serial No. 09/189,103, filed November 9, 1998; U.S. patent application Serial No. 08/650,400, filed May 20, 1996, now U.S. Patent No. 5,837,458; U.S. patent application Serial No. 08/621,430, filed